SEQUENCE LISTING

<110> Presnell, Scott R.
Kuestner, Rolf E.
Gao, Zeren

<120> Human Cytokine Receptor

<130> 00-49

<160> 13

<170> FastSEQ for Windows Version 3.0

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<213> Homo sapiens

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<222> (86)...(2344)

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                             Met Ala Pro Trp Leu Gln Leu Cys Ser
                              1               5

gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg      160
Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val
 10                  15                  20                  25

gcc gct ggc ggg tcc ggc cgc gcg cgg ggc gcc gac acc tgt ggc tgg      208
Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp
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agg atg aaa gcg gct gcc cga ccc cgg ctt tgt gtt gct aat gag gga      256
Arg Met Lys Ala Ala Ala Arg Pro Arg Leu Cys Val Ala Asn Glu Gly
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Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile
     75                  80                  85

gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat gac caa      400
Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln
 90                  95                 100                 105

gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc      448
Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe
                110                 115                 120

ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga      496
Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg
            125                 130                 135

cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac agt agc      544
Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser
        140                 145                 150

ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg aaa ttt      592
Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe
    155                 160                 165

gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att aaa aac      640
Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn
170                 175                 180                 185

gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt gac ctg      688
Glu Ser Asn Tyr His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu
                190                 195                 200

ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag cct cgg      736
Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg
            205                 210                 215

aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc ttc gac      784
Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp
        220                 225                 230
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cat gca ccg cac aac ttc ggc ttc cgt ttc ttc tat ctt cac tac aag      832
His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys
    235                 240                 245

ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag gag caa      880
Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln
250                 255                 260                 265

act aca gag acg acc agc tgc ctc ctt caa aat gtt tct cca ggg gat      928
Thr Thr Glu Thr Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp
                270                 275                 280

tat ata att gag ctg gtg gat gac act aac aca aca aga aaa gtg atg      976
Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met
            285                 290                 295

cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga     1024
His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg
        300                 305                 310

gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg     1072
Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr
    315                 320                 325

ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata tat tca     1120
Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser
330                 335                 340                 345

cat tta gat gaa gag agc tct gag tct tcc aca tac act gca gca ctc     1168
His Leu Asp Glu Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu
                350                 355                 360

cca aga gag agg ctc cgg ccg cgg ccg aag gtc ttt ctc tgc tat tcc     1216
Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser
            365                 370                 375

agt aaa gat ggc cag aat cac atg aat gtc gtc cag tgt ttc gcc tac     1264
Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr
        380                 385                 390

ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa     1312
Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu
    395                 400                 405
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```
gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag      1360
Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys
410                 415                 420                 425

atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag      1408
Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys
                430                 435                 440

tac ttt gtg gac aag aag aac tac aaa cac aaa gga ggt ggc cga ggc      1456
Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly
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tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa      1504
Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu
        460                 465                 470

aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt      1552
Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe
    475                 480                 485

atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc      1600
Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile
490                 495                 500                 505

cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct cag ctc      1648
Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu
                510                 515                 520

tgt tcc cac ttg cac tcc cga gac cac ggc ctc cag gag ccg ggg cag      1696
Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln
            525                 530                 535

cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag tca ggc      1744
His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly
        540                 545                 550

cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att gac gag      1792
Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu
    555                 560                 565

gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca      1840
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Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro
570                 575                 580                 585

ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt     1888
Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val
                590                 595                 600

tta aat gat gtc atg tgc aaa cca ggg cct gag agt gac ttc tgc cta     1936
Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu
            605                 610                 615

aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac tcc cag     1984
Lys Val Glu Ala Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln
        620                 625                 630

cac gag agt cag cat ggg ggc ctg gac caa gac ggg gag gcc cgg cct     2032
His Glu Ser Gln His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro
    635                 640                 645

gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa     2080
Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys
650                 655                 660                 665

gcc ggc agc ccc tcg gac atg ccg cgg gac tca ggc atc tat gac tcg     2128
Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser
                670                 675                 680

tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg     2176
Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser
            685                 690                 695

acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct     2224
Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser
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tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc     2272
Ser Gly Leu Gly Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu
    715                 720                 725

tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac act gat     2320
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gaa ctc cac gcg gtc gcc cct ttg taacaaaacg aaagagtcta agcattgcca    2374
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<213> Homo sapiens

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Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Met Lys Ala Ala Ala Arg
        35                  40                  45
Pro Arg Leu Cys Val Ala Asn Glu Gly Val Gly Pro Ala Ser Arg Asn
    50                  55                  60
Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr
65                  70                  75                  80
Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr
                85                  90                  95
Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp
            100                 105                 110
Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile
        115                 120                 125
Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu
    130                 135                 140
Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu
145                 150                 155                 160
Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys
                165                 170                 175
Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe
            180                 185                 190
Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu
        195                 200                 205
Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His
    210                 215                 220
Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly
225                 230                 235                 240
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Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe
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Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Thr Thr Ser Cys
            260                 265                 270
Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp
        275                 280                 285
Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro Val
    290                 295                 300
His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro
305                 310                 315                 320
Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg
                325                 330                 335
Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Ser
            340                 345                 350
Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg Pro
        355                 360                 365
Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn His
    370                 375                 380
Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly
385                 390                 395                 400
Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu
                405                 410                 415
Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe Ile
            420                 425                 430
Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn
        435                 440                 445
Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu Phe
    450                 455                 460
Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln
465                 470                 475                 480
Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp Tyr
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Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys Tyr
            500                 505                 510
Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser Arg
        515                 520                 525
Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg
    530                 535                 540
Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile
545                 550                 555                 560
Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys
                565                 570                 575
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Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro Val
            580                 585                 590
Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys Lys
        595                 600                 605
Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val Leu
    610                 615                 620
Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly Gly
625                 630                 635                 640
Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala Ala
                645                 650                 655
Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp Met
            660                 665                 670
Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu
        675                 680                 685
Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr Ser
    690                 695                 700
Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu Glu
705                 710                 715                 720
Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys Ala
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Leu
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<210> 3
<211> 2259
<212> DNA
<213> Artificial Sequence

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<221> misc_feature
<222> (1)...(2259)
<223> n = A,T,C or G

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wsncarytng cngtngcngc nggnggnwsn ggnmgngcnm gnggngcnga yacntgyggn     120
tggmgnatga argcngcngc nmgnccnmgn ytntgygtng cnaaygargg ngtnggnccn     180
gcnwsnmgna aywsnggnyt ntayaayath acnttyaart aygayaaytg yacnacntay     240
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ytnaayccng tnggnaarca ygtnathgcn gaygcncara ayathacnat hwsncartay 300
gcntgycayg aycargtngc ngtnacnath ytntggwsnc cnggngcnyt nggnathgar 360
ttyytnaarg gnttymgngt nathytngar garytnaarw sngarggnmg ncartgycar 420
carytnathy tnaargaycc naarcarytn aaywsnwsnt tyaarmgnac nggnatggar 480
wsncarccnt tyytnaayat gaarttygar acngaytayt tygtnaargt ngtnccntty 540
ccnwsnatha araaygarws naaytaycay ccnttyttyt tymgnacnmg ngcntgygay 600
ytnytnytnc arccngayaa yytngcntgy aarccnttyt ggaarccnmg naayytnaay 660
athwsncarc ayggnwsnga yatgcargtn wsnttygayc aygcnccnca yaayttyggn 720
ttymgnttyt tytayytnca ytayaarytn aarcaygarg gnccnttyaa rmgnaaracn 780
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acngaracnw snwsnytnac ngarwsngtn wsnwsnwsnw snggnytngg ngargargar 2160
ccnccngcny tnccnwsnaa rytnytnwsn wsnggnwsnt gyaargcnga yytnggntgy 2220
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<220>
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<222> (86)...(2344)

<400> 4

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ggcctggctg ggcgagcgca cggcc atg gcc ccg tgg ctg cag ctc tgc tcc      112
                             Met Ala Pro Trp Leu Gln Leu Cys Ser
                              1               5

gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg      160
Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val
 10                  15                  20                  25

gcc gct ggc ggg tcc ggc cgc gcg cgg ggc gcc gac acc tgt ggc tgg      208
Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp
                 30                  35                  40

agg atg aaa gcg gct gcc cga ccc cgg ctt tgt gtt gct aat gag gga      256
Arg Met Lys Ala Ala Ala Arg Pro Arg Leu Cys Val Ala Asn Glu Gly
             45                  50                  55

gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa      304
Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys
         60                  65                  70

tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att      352
Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile
     75                  80                  85

gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat gac caa      400
Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln
 90                  95                 100                 105

gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc      448
Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe
                110                 115                 120

ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga      496
Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg
            125                 130                 135

cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac agt agc      544
Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser
        140                 145                 150
```

```
ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg aaa ttt      592
Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe
    155                 160                 165

gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att aaa aac      640
Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn
170                 175                 180                 185

gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt gac ctg      688
Glu Ser Asn Tyr His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu
            190                 195                 200

ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag cct cgg      736
Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg
            205                 210                 215

aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc ttc gac      784
Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp
        220                 225                 230

cac gca ccg cac aac ttc ggc ttc cgt ttc ttc tat ctt cac tac aag      832
His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys
    235                 240                 245

ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag gag caa      880
Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln
250                 255                 260                 265

act aca gag atg acc agc tgc ctc ctt caa aat gtt tct cca ggg gat      928
Thr Thr Glu Met Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp
                270                 275                 280

tat ata att gag ctg gtg gat gac act aac aca aca aga aaa gtg atg      976
Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met
            285                 290                 295

cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga     1024
His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg
        300                 305                 310

gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg     1072
Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr
    315                 320                 325
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ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata tat tca     1120
Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser
330                 335                 340                 345

cat tta gat gaa gag agc tct gag tct tcc aca tac act gca gca ctc     1168
His Leu Asp Glu Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu
                350                 355                 360

cca aga gag agg ctc cgg ccg cgg ccg aag gtc ttt ctc tgc tat tcc     1216
Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser
            365                 370                 375

agt aaa gat ggc cag aat cac atg aat gtc gtc cag tgt ttc gcc tac     1264
Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr
        380                 385                 390

ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa     1312
Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu
    395                 400                 405

gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag     1360
Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys
410                 415                 420                 425

atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag     1408
Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys
                430                 435                 440

tac ttt gtg gac aag aag aac tac aaa cac aaa gga ggt ggc cga ggc     1456
Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly
            445                 450                 455

tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa     1504
Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu
        460                 465                 470

aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt     1552
Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe
    475                 480                 485

atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc     1600
```

```
Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile
490                 495                 500                 505

cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct cag ctc    1648
Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu
                510                 515                 520

tgt tcc cac ctg cac tcc cga gac cac ggc ctc cag gag ccg ggg cag    1696
Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln
            525                 530                 535

cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag tca ggc    1744
His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly
        540                 545                 550

cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att gac gag    1792
Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu
    555                 560                 565

gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca    1840
Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro
570                 575                 580                 585

ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt    1888
Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val
                590                 595                 600

tta aat gat gtc atg tgc aaa cca ggg cct gag agt gac ttc tgc cta    1936
Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu
            605                 610                 615

aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac tcc cag    1984
Lys Val Glu Ala Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln
        620                 625                 630

cac gag agt cag cat ggg ggc ctg gac caa gac ggg gag gcc cgg cct    2032
His Glu Ser Gln His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro
    635                 640                 645

gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa    2080
Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys
650                 655                 660                 665
```

```
gcc ggc agc ccc tcg gac atg ccg cgg gac tca ggc atc tat gac tcg     2128
Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser
                670                 675                 680

tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg     2176
Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser
            685                 690                 695

acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct     2224
Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser
        700                 705                 710

tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc     2272
Ser Gly Leu Gly Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu
    715                 720                 725

tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac act gat     2320
Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp
730                 735                 740                 745

gaa ctc cac gcg gcc gcc cct ttg taacaaaacg aaagagtcta agcattgcca     2374
Glu Leu His Ala Ala Ala Pro Leu
                750

ctttagctg                                                           2383
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<210> 5
<211> 753
<212> PRT
<213> Homo sapiens

<400> 5

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Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn Ala
 1               5                  10                  15
Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg
            20                  25                  30
Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Met Lys Ala Ala Ala Arg
        35                  40                  45
Pro Arg Leu Cys Val Ala Asn Glu Gly Val Gly Pro Ala Ser Arg Asn
    50                  55                  60
Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr
65                  70                  75                  80
```

```
Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr
                85                  90                  95
Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp
            100                 105                 110
Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile
        115                 120                 125
Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu
    130                 135                 140
Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu
145                 150                 155                 160
Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys
                165                 170                 175
Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe
            180                 185                 190
Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu
        195                 200                 205
Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His
    210                 215                 220
Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly
225                 230                 235                 240
Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe
                245                 250                 255
Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr Ser Cys
            260                 265                 270
Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp
        275                 280                 285
Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro Val
    290                 295                 300
His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro
305                 310                 315                 320
Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg
                325                 330                 335
Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Ser
            340                 345                 350
Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg Pro
        355                 360                 365
Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn His
    370                 375                 380
Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly
385                 390                 395                 400
Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu
                405                 410                 415
```

Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe Ile
420 425 430
Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn
435 440 445
Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu Phe
450 455 460
Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln
465 470 475 480
Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp Tyr
485 490 495
Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys Tyr
500 505 510
Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser Arg
515 520 525
Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg
530 535 540
Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile
545 550 555 560
Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys
565 570 575
Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro Val
580 585 590
Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys Lys
595 600 605
Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val Leu
610 615 620
Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly Gly
625 630 635 640
Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala Ala
645 650 655
Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp Met
660 665 670
Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu
675 680 685
Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr Ser
690 695 700
Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu Glu
705 710 715 720
Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys Ala
725 730 735
Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Ala Ala Pro
740 745 750

Leu

<210> 6
<211> 2259
<212> DNA
<213> Artificial Sequence

<220>
<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:5.

<221> misc_feature
<222> (1)...(2259)
<223> n = A,T,C or G

<400> 6

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atggcnccnt ggytncaryt ntgywsngtn ttyttyacng tnaaygcntg yytnaayggn     60
wsncarytng cngtngcngc nggnggnwsn ggnmgngcnm gnggngcnga yacntgyggn    120
tggmgnatga argcngcngc nmgnccnmgn ytntgygtng cnaaygargg ngtnggnccn    180
gcnwsnmgna aywsnggnyt ntayaayath acnttyaart aygayaaytg yacnacntay    240
ytnaayccng tnggnaarca ygtnathgcn gaygcncara ayathacnat hwsncartay    300
gcntgycayg aycargtngc ngtnacnath ytntggwsnc cnggngcnyt nggnathgar    360
ttyytnaarg gnttymgngt nathytngar garytnaarw sngarggnmg ncartgycar    420
carytnathy tnaargaycc naarcarytn aaywsnwsnt tyaarmgnac nggnatggar    480
wsncarccnt tyytnaayat gaarttygar acngaytayt tygtnaargt ngtnccntty    540
ccnwsnatha araaygarws naaytaycay ccnttyttyt tymgnacnmg ngcntgygay    600
ytnytnytnc arccngayaa yytngcntgy aarccnttyt ggaarccnmg naayytnaay    660
athwsncarc ayggnwsnga yatgcargtn wsnttygayc aygcnccnca yaayttyggn    720
ttymgnttyt tytayytnca ytayaarytn aarcaygarg gnccnttyaa rmgnaaracn    780
tgyaarcarg arcaracnac ngaratgacn wsntgyytny tncaraaygt nwsnccnggn    840
gaytayatha thgarytngt ngaygayacn aayacnacnm gnaargtnat gcaytaygcn    900
ytnaarccng tncaywsncc ntgggcnggn ccnathmgng cngtngcnat hacngtnccn    960
ytngtngtna thwsngcntt ygcnacnytn ttyacngtna tgtgymgnaa raarcarcar   1020
garaayatht aywsncayyt ngaygargar wsnwsngarw snwsnacnta yacngcngcn   1080
ytnccnmgng armgnytnmg nccnmgnccn aargtnttyy tntgytayws nwsnaargay   1140
ggncaraayc ayatgaaygt ngtncartgy ttygcntayt tyytncarga yttytgyggn   1200
tgygargtng cnytngayyt ntgggargay ttywsnytnt gymgngargg ncarmgngar   1260
tgggtnathc araarathca ygarwsncar ttyathathg tngtntgyws naarggnatg   1320
aartayttyg tngayaaraa raaytayaar cayaarggng gnggnmgngg nwsnggnaar   1380
ggngarytnt tyytngtngc ngtnwsngcn athgcngara arytnmgnca rgcnaarcar   1440
wsnwsnwsng cngcnytnws naarttyath gcngtntayt tygaytayws ntgygarggn   1500
gaygtnccng gnathytnga yytnwsnacn aartaymgny tnatggayaa yytnccncar   1560
ytntgywsnc ayytncayws nmgngaycay ggnytncarg arccnggnca rcayacnmgn   1620
```

```
carggnwsnm gnmgnaayta yttymgnwsn aarwsnggnm gnwsnytnta ygtngcnath    1680
tgyaayatgc aycarttyat hgaygargar ccngaytggt tygaraarca rttygtnccn    1740
ttycayccnc cnccnytnmg ntaymgngar ccngtnytng araarttyga ywsnggnytn    1800
gtnytnaayg aygtnatgtg yaarccnggn ccngarwsng ayttytgyyt naargtngar    1860
gcngcngtny tnggngcnac nggnccngcn gaywsncarc aygarwsnca rcayggnggn    1920
ytngaycarg ayggngargc nmgnccngcn ytngayggnw sngcngcnyt ncarccnytn    1980
ytncayacng tnaargcngg nwsnccnwsn gayatgccnm gngaywsngg nathtaygay    2040
wsnwsngtnc cnwsnwsnga rytnwsnytn ccnytnatgg arggnytnws nacngaycar    2100
acngaracnw snwsnytnac ngarwsngtn wsnwsnwsnw snggnytngg ngargargar    2160
ccnccngcny tnccnwsnaa rytnytnwsn wsnggnwsnt gyaargcnga yytnggntgy    2220
mgnwsntaya cngaygaryt ncaygcngcn gcnccnytn                           2259
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<210> 7
<211> 2341
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (86)...(2302)

<400> 7

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ccgccgcggc caccgcccac tcggggctgg ccagcggcgg gcggccgggg cgcagagaac     60
ggcctggctg ggcgagcgca cggcc atg gcc ccg tgg ctg cag ctc tgc tcc      112
                            Met Ala Pro Trp Leu Gln Leu Cys Ser
                             1               5

gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg      160
Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val
 10                  15                  20                  25

gcc gct ggc ggg tcc ggc cgc gcg cgg ggc gcc gac acc tgt ggc tgg      208
Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp
                 30                  35                  40

agg gga gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc      256
Arg Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr
             45                  50                  55

ttc aaa tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat      304
Phe Lys Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His
         60                  65                  70
```

```
gtg att gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat      352
Val Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His
     75                  80                  85

gac caa gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc      400
Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile
 90                  95                 100                 105

gaa ttc ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag      448
Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu
                110                 115                 120

gga aga cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac      496
Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn
            125                 130                 135

agt agc ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg      544
Ser Ser Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met
        140                 145                 150

aaa ttt gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att      592
Lys Phe Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile
    155                 160                 165

aaa aac gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt      640
Lys Asn Glu Ser Asn Tyr His Pro Phe Phe Phe Arg Thr Arg Ala Cys
170                 175                 180                 185

gac ctg ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag      688
Asp Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys
                190                 195                 200

cct cgg aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc      736
Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser
            205                 210                 215

ttc gac cat gca ccg cac aac ttc ggc ttc cgt ttc ttc tat ctt cac      784
Phe Asp His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His
        220                 225                 230

tac aag ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag      832
Tyr Lys Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln
    235                 240                 245
```

gag caa act aca gag acg acc agc tgc ctc ctt caa aat gtt tct cca 880
Glu Gln Thr Thr Glu Thr Thr Ser Cys Leu Leu Gln Asn Val Ser Pro
250 255 260 265

ggg gat tat ata att gag ctg gtg gat gac act aac aca aca aga aaa 928
Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys
270 275 280

gtg atg cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc 976
Val Met His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro
285 290 295

atc aga gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc 1024
Ile Arg Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe
300 305 310

gcg acg ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata 1072
Ala Thr Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile
315 320 325

tat tca cat tta gat gaa gag agc tct gag tct tcc aca tac act gca 1120
Tyr Ser His Leu Asp Glu Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala
330 335 340 345

gca ctc cca aga gag agg ctc cgg ccg cgg ccg aag gtc ttt ctc tgc 1168
Ala Leu Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys
350 355 360

tat tcc agt aaa gat ggc cag aat cac atg aat gtc gtc cag tgt ttc 1216
Tyr Ser Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe
365 370 375

gcc tac ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg 1264
Ala Tyr Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu
380 385 390

tgg gaa gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc 1312
Trp Glu Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile
395 400 405

cag aag atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt 1360

```
Gln Lys Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly
410                 415                 420                 425

atg aag tac ttt gtg gac aag aag aac tac aaa cac aaa gga ggt ggc    1408
Met Lys Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Gly
                430                 435                 440

cga ggc tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att    1456
Arg Gly Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile
            445                 450                 455

gcc gaa aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc    1504
Ala Glu Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser
        460                 465                 470

aag ttt atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc    1552
Lys Phe Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro
    475                 480                 485

ggt atc cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct    1600
Gly Ile Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro
490                 495                 500                 505

cag ctc tgt tcc cac ttg cac tcc cga gac cac ggc ctc cag gag ccg    1648
Gln Leu Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro
                510                 515                 520

ggg cag cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag    1696
Gly Gln His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys
            525                 530                 535

tca ggc cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att    1744
Ser Gly Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile
        540                 545                 550

gac gag gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct    1792
Asp Glu Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro
    555                 560                 565

cct cca ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc    1840
Pro Pro Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly
570                 575                 580                 585
```

```
ttg gtt tta aat gat gtc atg tgc aaa cca ggg cct gag agt gac ttc      1888
Leu Val Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe
                590                 595                 600

tgc cta aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac      1936
Cys Leu Lys Val Glu Ala Ala Val Leu Gly Ala Thr Gly Pro Ala Asp
            605                 610                 615

tcc cag cac gag agt cag cat ggg ggc ctg gac caa gac ggg gag gcc      1984
Ser Gln His Glu Ser Gln His Gly Gly Leu Asp Gln Asp Gly Glu Ala
        620                 625                 630

cgg cct gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg      2032
Arg Pro Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr
    635                 640                 645

gtg aaa gcc ggc agc ccc tcg gac atg ccg cgg gac tca ggc atc tat      2080
Val Lys Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr
650                 655                 660                 665

gac tcg tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga      2128
Asp Ser Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly
                670                 675                 680

ctc tcg acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc      2176
Leu Ser Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser
            685                 690                 695

tcc tct tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag      2224
Ser Ser Ser Gly Leu Gly Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys
        700                 705                 710

ctc ctc tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac      2272
Leu Leu Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr
    715                 720                 725

act gat gaa ctc cac gcg gtc gcc cct ttg taacaaaacg aaagagtcta      2322
Thr Asp Glu Leu His Ala Val Ala Pro Leu
730                 735

agcattgcca ctttagctg                                               2341
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<210> 8
<211> 739
<212> PRT
<213> Homo sapiens

<400> 8

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Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn Ala
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Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg
            20                  25                  30
Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser
        35                  40                  45
Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr
    50                  55                  60
Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn
65                  70                  75                  80
Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile
                85                  90                  95
Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg
            100                 105                 110
Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu
        115                 120                 125
Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly
    130                 135                 140
Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe
145                 150                 155                 160
Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His
                165                 170                 175
Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp
            180                 185                 190
Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser
        195                 200                 205
Gln His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn
    210                 215                 220
Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly
225                 230                 235                 240
Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Thr Thr
                245                 250                 255
Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu
            260                 265                 270
Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys
        275                 280                 285
```

```
Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr
    290                 295                 300
Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met
305                 310                 315                 320
Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu
                325                 330                 335
Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu
            340                 345                 350
Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln
        355                 360                 365
Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe
    370                 375                 380
Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys
385                 390                 395                 400
Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln
                405                 410                 415
Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys
            420                 425                 430
Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu
        435                 440                 445
Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala
    450                 455                 460
Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe
465                 470                 475                 480
Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr
                485                 490                 495
Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His
            500                 505                 510
Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly
        515                 520                 525
Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val
    530                 535                 540
Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe
545                 550                 555                 560
Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu
                565                 570                 575
Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met
            580                 585                 590
Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala
        595                 600                 605
Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His
    610                 615                 620
```

```
Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser
625                 630                 635                 640
Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser
                645                 650                 655
Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser
            660                 665                 670
Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu
        675                 680                 685
Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu
    690                 695                 700
Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys
705                 710                 715                 720
Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val
                725                 730                 735
Ala Pro Leu
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<210> 9
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:8.

<221> misc_feature
<222> (1)...(2217)
<223> n = A,T,C or G

<400> 9

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wsncarytng cngtngcngc nggnggnwsn ggnmgngcnm gnggngcnga yacntgyggn    120
tggmgnggng tnggnccngc nwsnmgnaay wsnggnytnt ayaayathac nttyaartay    180
gayaaytgya cnacntayyt naayccngtn ggnaarcayg tnathgcnga ygcncaraay    240
athacnathw sncartaygc ntgycaygay cargtngcng tnacnathyt ntggwsnccn    300
ggngcnytng gnathgartt yytnaarggn ttymgngtna thytngarga rytnaarwsn    360
garggnmgnc artgycarca rytnathytn aargayccna arcarytnaa ywsnwsntty    420
aarmgnacng gnatggarws ncarccntty ytnaayatga arttygarac ngaytaytty    480
gtnaargtng tnccnttycc nwsnathaar aaygarwsna aytaycaycc nttyttytty    540
mgnacnmgng cntgygayyt nytnytncar ccngayaayy tngcntgyaa rccnttytgg    600
aarccnmgna ayytnaayat hwsncarcay ggnwsngaya tgcargtnws nttygaycay    660
gcnccncaya ayttyggntt ymgnttytty tayytncayt ayaarytnaa rcaygarggn    720
ccnttyaarm gnaaracntg yaarcargar caracnacng aracnacnws ntgyytnytn    780
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caraaygtnw snccnggnga ytayathath garytngtng aygayacnaa yacnacnmgn 840
aargtnatgc aytaygcnyt naarccngtn caywsnccnt gggcnggncc nathmgngcn 900
gtngcnatha cngtnccnyt ngtngtnath wsngcnttyg cnacnytntt yacngtnatg 960
tgymgnaara arcarcarga raayathtay wsncayytng aygargarws nwsngarwsn 1020
wsnacntaya cngcngcnyt nccnmgngar mgnytnmgnc cnmgnccnaa rgtnttyytn 1080
tgytaywsnw snaargaygg ncaraaycay atgaaygtng tncartgytt ygcntaytty 1140
ytncargayt tytgyggntg ygargtngcn ytngayytnt gggargaytt ywsnytntgy 1200
mgngarggnc armgngartg ggtnathcar aarathcayg arwsncartt yathathgtn 1260
gtntgywsna arggnatgaa rtayttygtn gayaaraara aytayaarca yaarggnggn 1320
ggnmgnggnw snggnaargg ngarytntty ytngtngcng tnwsngcnat hgcngaraar 1380
ytnmgncarg cnaarcarws nwsnwsngcn gcnytnwsna arttyathgc ngtntaytty 1440
gaytaywsnt gygarggnga ygtnccnggn athytngayy tnwsnacnaa rtaymgnytn 1500
atggayaayy tnccncaryt ntgywsncay ytncaywsnm gngaycaygg nytncargar 1560
ccnggncarc ayacnmgnca rggnwsnmgn mgnaaytayt tymgnwsnaa rwsnggnmgn 1620
wsnytntayg tngcnathtg yaayatgcay carttyathg aygargarcc ngaytggtty 1680
garaarcart tygtnccntt ycayccnccn ccnytnmgnt aymgngarcc ngtnytngar 1740
aarttygayw snggnytngt nytnaaygay gtnatgtgya arccnggncc ngarwsngay 1800
ttytgyytna argtngargc ngcngtnytn ggngcnacng gnccngcnga ywsncarcay 1860
garwsncarc ayggnggnyt ngaycargay ggngargcnm gnccngcnyt ngayggnwsn 1920
gcngcnytnc arccnytnyt ncayacngtn aargcnggnw snccnwsnga yatgccnmgn 1980
gaywsnggna thtaygayws nwsngtnccn wsnwsngary tnwsnytncc nytnatggar 2040
ggnytnwsna cngaycarac ngaracnwsn wsnytnacng arwsngtnws nwsnwsnwsn 2100
ggnytnggng argargarcc nccngcnytn ccnwsnaary tnytnwsnws nggnwsntgy 2160
aargcngayy tnggntgymg nwsntayacn gaygarytnc aygcngtngc nccnytn 2217

<210> 10
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide linker.

<400> 10
Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 11
<211> 2443
<212> DNA
<213> Mouse

<220>

<221> CDS
<222> (101)...(2317)

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aacctagcgg agaccggccc aactgggcga gcgtacggcc atg gcc ccg tgg ctg 115
Met Ala Pro Trp Leu
1 5

cag ctc tgc tcc ttc ttc ttc act gtc aac gcc tgt ctc aac ggc tcg 163
Gln Leu Cys Ser Phe Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser
10 15 20

cag ctg gca gtg gcc gcg ggc ggc tcc ggc cgc gcg agg ggc gcg gac 211
Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp
25 30 35

acc tgt ggc tgg agg gga gtg ggg ccg gcc agc agg aac agc gga ctg 259
Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu
40 45 50

cac aac atc acc ttc aga tac gac aac tgt acc acc tac ttg aat ccc 307
His Asn Ile Thr Phe Arg Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro
55 60 65

ggc ggc ggg aag cat gcg att gct gat gct cag aac atc acc atc agc 355
Gly Gly Gly Lys His Ala Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser
70 75 80 85

cag tac gct tgc cac gac cag gtg gca gtc acc att ctt tgg tcc cca 403
Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro
90 95 100

ggg gcc ctt ggc att gaa ttc cta aaa gga ttc cga gtc atc ctg gag 451
Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu
105 110 115

gag ctg aag tcg gag ggc aga cag tgc caa cag ctg att cta aag gac 499
Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp
120 125 130

ccc aaa cag ctc aac agc agc ttc aga agg act gga atg gaa tct cag 547

```
Pro Lys Gln Leu Asn Ser Ser Phe Arg Arg Thr Gly Met Glu Ser Gln
    135                 140                 145

cct ttc ctg aat atg aaa ttt gag acg gat tac ttt gta aag att gtc      595
Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys Ile Val
150                 155                 160                 165

cct ttc cct tcc att aaa aat gaa agc aat tac cat ccc ttc ttc ttc      643
Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe Phe Phe
                170                 175                 180

aga aca cgg gcc tgt gac ctg ttg tta caa cct gac aac ttg gcc tgt      691
Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys
            185                 190                 195

aag cct ttc tgg aag cct cga aac ctg aat atc agc cag cat ggt tct      739
Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser
        200                 205                 210

gac atg cac gtg tcc ttc gac cat gcc ccg cag aac ttc ggc ttc cgt      787
Asp Met His Val Ser Phe Asp His Ala Pro Gln Asn Phe Gly Phe Arg
    215                 220                 225

ggc ttc cat gtt ctc tat aag ctc aag cac gaa ggc ccc ttc agg cgg      835
Gly Phe His Val Leu Tyr Lys Leu Lys His Glu Gly Pro Phe Arg Arg
230                 235                 240                 245

agg act tgc agg cag gac cag aat aca gag aca acc agc tgc ctc ctc      883
Arg Thr Cys Arg Gln Asp Gln Asn Thr Glu Thr Thr Ser Cys Leu Leu
                250                 255                 260

caa aac gtt tct cca ggg gac tat atc att gag ctg gtg gat gac agc      931
Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Ser
            265                 270                 275

aac acc acc agg aaa gct gct cag tat gtg gtg aag tca gtg cag tct      979
Asn Thr Thr Arg Lys Ala Ala Gln Tyr Val Val Lys Ser Val Gln Ser
        280                 285                 290

ccc tgg gct gga ccc atc aga gct gtg gcc atc act gtg cct ctg gtt     1027
Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro Leu Val
    295                 300                 305
```

```
gtc ata tct gcg ttc gca acc ctg ttc act gtg atg tgc aga aag aag     1075
Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg Lys Lys
310                 315                 320                 325

caa caa gaa aat ata tat tca cat tta gat gaa gaa agc ccg gag tcg     1123
Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Pro Glu Ser
                330                 335                 340

tcc aca tac gct gcg gct ctc ccc aga gac agg ctc cgg cct cag ccc     1171
Ser Thr Tyr Ala Ala Ala Leu Pro Arg Asp Arg Leu Arg Pro Gln Pro
            345                 350                 355

aag gtc ttc ctc tgc tac tcc aat aaa gat ggc cag aat cac atg aac     1219
Lys Val Phe Leu Cys Tyr Ser Asn Lys Asp Gly Gln Asn His Met Asn
        360                 365                 370

gtg gtc cag tgt ttc gcc tat ttc ctg caa gat ttc tgt ggc tgt gag     1267
Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly Cys Glu
    375                 380                 385

gtg gct ctg gac ttg tgg gaa gat ttc agc ctc tgc aga gag ggg cag     1315
Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu Gly Gln
390                 395                 400                 405

aga gaa tgg gcc att cag aag atc cac gag tcc cag ttc atc att gtc     1363
Arg Glu Trp Ala Ile Gln Lys Ile His Glu Ser Gln Phe Ile Ile Val
                410                 415                 420

gtg tgc tcc aaa ggc atg aag tac ttt gta gat aag aag aac ttc aga     1411
Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn Phe Arg
            425                 430                 435

cac aaa gga ggc agc cgc ggc gag gcg caa ggc gag ttc ttc ctg gtg     1459
His Lys Gly Gly Ser Arg Gly Glu Ala Gln Gly Glu Phe Phe Leu Val
        440                 445                 450

gcc gtg gca gcc att gct gag aag ctc cgt cag gcc aag cag agc tca     1507
Ala Val Ala Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln Ser Ser
    455                 460                 465

tct gcc gca ctg cgc aag ttc atc gcc gtc tac ttc gat tat tcc tgt     1555
```

```
Ser Ala Ala Leu Arg Lys Phe Ile Ala Val Tyr Phe Asp Tyr Ser Cys
470                 475                 480                 485

gaa ggg gat gta ccc tgc agc ctg gac ctg agc acc aag tac aag ctc    1603
Glu Gly Asp Val Pro Cys Ser Leu Asp Leu Ser Thr Lys Tyr Lys Leu
                490                 495                 500

atg gac cac ctt cct gag ctc tgt gcc cat ctg cac tca gga gag cag    1651
Met Asp His Leu Pro Glu Leu Cys Ala His Leu His Ser Gly Glu Gln
            505                 510                 515

gag gtg ctg ggt cag cac cca ggc cac agc agc aga agg aac tac ttc    1699
Glu Val Leu Gly Gln His Pro Gly His Ser Ser Arg Arg Asn Tyr Phe
        520                 525                 530

cgg agc aaa tcg ggc cgc tcc ctg tat gtt gcc att tgc aac atg cac    1747
Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His
    535                 540                 545

cag ttt att gat gag gag cct gac tgg ttt gag aag cag ttt ata ccc    1795
Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys Gln Phe Ile Pro
550                 555                 560                 565

ttc caa cat ccc cct gtg cgc tac cag gag cca gtc ctg gag aaa ttt    1843
Phe Gln His Pro Pro Val Arg Tyr Gln Glu Pro Val Leu Glu Lys Phe
                570                 575                 580

gac tca ggc ttg gtt tta aat gat gtc ata agc aaa cca ggg cca gag    1891
Asp Ser Gly Leu Val Leu Asn Asp Val Ile Ser Lys Pro Gly Pro Glu
            585                 590                 595

agt gac ttc tgt cgg aaa gtc gag gct tgt gta ctt ggg gcc gct ggg    1939
Ser Asp Phe Cys Arg Lys Val Glu Ala Cys Val Leu Gly Ala Ala Gly
        600                 605                 610

cca gcc gac tct tat tca tac ctg gag agt cag cat gta ggc ctg gac    1987
Pro Ala Asp Ser Tyr Ser Tyr Leu Glu Ser Gln His Val Gly Leu Asp
    615                 620                 625

caa gac act gag gcc cag ccc tcc tgt gat agt gcc cct gcc ttg cag    2035
Gln Asp Thr Glu Ala Gln Pro Ser Cys Asp Ser Ala Pro Ala Leu Gln
630                 635                 640                 645
```

```
ccc ctg tta cac gca gtg aaa gct ggc agt ccc tca gag atg cca cgg     2083
Pro Leu Leu His Ala Val Lys Ala Gly Ser Pro Ser Glu Met Pro Arg
                650                 655                 660

gac tca ggc ata tat gat tct tct gta ccc tca tca gag ctc tct ctg     2131
Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu Ser Leu
            665                 670                 675

cct ctg atg gag gga ctc tcc ccg gat cag ata gaa aca tct tct ctg     2179
Pro Leu Met Glu Gly Leu Ser Pro Asp Gln Ile Glu Thr Ser Ser Leu
        680                 685                 690

acc gag agt gta tct tcc tcc tct ggc cta ggt gag gag gac ccc cct     2227
Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu Asp Pro Pro
    695                 700                 705

acc ctc cct tcc aag ctc ttt gcc tct ggg gtg tcc aga gaa cat ggt     2275
Thr Leu Pro Ser Lys Leu Phe Ala Ser Gly Val Ser Arg Glu His Gly
710                 715                 720                 725

tgc cac agc cac act gac gaa ctg caa gcg ctt gct cct ttg              2317
Cys His Ser His Thr Asp Glu Leu Gln Ala Leu Ala Pro Leu
                730                 735

taaggactcg gaagagtcta agcatcgcca ctttagctgc tgatctctct ggctccccag   2377
ttcacctctg tggttgtgca gcctacttgg agctgaaggc gcacacgggg atatctggaa   2437
tgaaat                                                              2443
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<210> 12
<211> 739
<212> PRT
<213> Mouse

<400> 12

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            20                  25                  30
Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser
        35                  40                  45
Arg Asn Ser Gly Leu His Asn Ile Thr Phe Arg Tyr Asp Asn Cys Thr
    50                  55                  60
```

Thr Tyr Leu Asn Pro Gly Gly Gly Lys His Ala Ile Ala Asp Ala Gln
65 70 75 80
Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr
85 90 95
Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe
100 105 110
Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln
115 120 125
Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Arg Arg Thr
130 135 140
Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr
145 150 155 160
Phe Val Lys Ile Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr
165 170 175
His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro
180 185 190
Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile
195 200 205
Ser Gln His Gly Ser Asp Met His Val Ser Phe Asp His Ala Pro Gln
210 215 220
Asn Phe Gly Phe Arg Gly Phe His Val Leu Tyr Lys Leu Lys His Glu
225 230 235 240
Gly Pro Phe Arg Arg Arg Thr Cys Arg Gln Asp Gln Asn Thr Glu Thr
245 250 255
Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu
260 265 270
Leu Val Asp Asp Ser Asn Thr Thr Arg Lys Ala Ala Gln Tyr Val Val
275 280 285
Lys Ser Val Gln Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile
290 295 300
Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val
305 310 315 320
Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu
325 330 335
Glu Ser Pro Glu Ser Ser Thr Tyr Ala Ala Ala Leu Pro Arg Asp Arg
340 345 350
Leu Arg Pro Gln Pro Lys Val Phe Leu Cys Tyr Ser Asn Lys Asp Gly
355 360 365
Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp
370 375 380
Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu
385 390 395 400

Cys Arg Glu Gly Gln Arg Glu Trp Ala Ile Gln Lys Ile His Glu Ser
405 410 415
Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp
420 425 430
Lys Lys Asn Phe Arg His Lys Gly Gly Ser Arg Gly Glu Ala Gln Gly
435 440 445
Glu Phe Phe Leu Val Ala Val Ala Ala Ile Ala Glu Lys Leu Arg Gln
450 455 460
Ala Lys Gln Ser Ser Ser Ala Ala Leu Arg Lys Phe Ile Ala Val Tyr
465 470 475 480
Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Cys Ser Leu Asp Leu Ser
485 490 495
Thr Lys Tyr Lys Leu Met Asp His Leu Pro Glu Leu Cys Ala His Leu
500 505 510
His Ser Gly Glu Gln Glu Val Leu Gly Gln His Pro Gly His Ser Ser
515 520 525
Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala
530 535 540
Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu
545 550 555 560
Lys Gln Phe Ile Pro Phe Gln His Pro Pro Val Arg Tyr Gln Glu Pro
565 570 575
Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Ile Ser
580 585 590
Lys Pro Gly Pro Glu Ser Asp Phe Cys Arg Lys Val Glu Ala Cys Val
595 600 605
Leu Gly Ala Ala Gly Pro Ala Asp Ser Tyr Ser Tyr Leu Glu Ser Gln
610 615 620
His Val Gly Leu Asp Gln Asp Thr Glu Ala Gln Pro Ser Cys Asp Ser
625 630 635 640
Ala Pro Ala Leu Gln Pro Leu Leu His Ala Val Lys Ala Gly Ser Pro
645 650 655
Ser Glu Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser
660 665 670
Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Pro Asp Gln Ile
675 680 685
Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly
690 695 700
Glu Glu Asp Pro Pro Thr Leu Pro Ser Lys Leu Phe Ala Ser Gly Val
705 710 715 720
Ser Arg Glu His Gly Cys His Ser His Thr Asp Glu Leu Gln Ala Leu
725 730 735

Ala Pro Leu

<210> 13
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:12.

<221> misc_feature
<222> (1)...(2217)
<223> n = A, T, C or G

<400> 13

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tggmgnggng tnggnccngc nwsnmgnaay wsnggnytnc ayaayathac nttymgntay    180
gayaaytgya cnacntayyt naayccnggn ggnggnaarc aygcnathgc ngaygcncar    240
aayathacna thwsncarta ygcntgycay gaycargtng cngtnacnat hytntggwsn    300
ccnggngcny tnggnathga rttyytnaar ggnttymgng tnathytnga rgarytnaar    360
wsngarggnm gncartgyca rcarytnath ytnaargayc cnaarcaryt naaywsnwsn    420
ttymgnmgna cnggnatgga rwsncarccn ttyytnaaya tgaarttyga racngaytay    480
ttygtnaara thgtnccntt yccnwsnath aaraaygarw snaaytayca yccnttytty    540
ttymgnacnm gngcntgyga yytnytnytn carccngaya ayytngcntg yaarccntty    600
tggaarccnm gnaayytnaa yathwsncar cayggnwsng ayatgcaygt nwsnttygay    660
caygcnccnc araayttygg nttymgnggn ttycaygtny tntayaaryt naarcaygar    720
ggnccnttym gnmgnmgnac ntgymgncar gaycaraaya cngaracnac nwsntgyytn    780
ytncaraayg tnwsnccngg ngaytayath athgarytng tngaygayws naayacnacn    840
mgnaargcng cncartaygt ngtnaarwsn gtncarwsnc cntgggcngg nccnathmgn    900
gcngtngcna thacngtncc nytngtngtn athwsngcnt tygcnacnyt nttyacngtn    960
atgtgymgna araarcarca rgaraayath taywsncayy tngaygarga rwsnccngar   1020
wsnwsnacnt aygcngcngc nytnccnmgn gaymgnytnm gnccncarcc naargtntty   1080
ytntgytayw snaayaarga yggncaraay cayatgaayg tngtncartg yttygcntay   1140
ttyytncarg ayttytgygg ntgygargtn gcnytngayy tntgggarga yttywsnytn   1200
tgymgngarg gncarmgnga rtgggcnath caraarathc aygarwsnca rttyathath   1260
gtngtntgyw snaarggnat gaartaytty gtngayaara araayttymg ncayaarggn   1320
ggnwsnmgng gngargcnca rggngartty ttyytngtng cngtngcngc nathgcngar   1380
aarytnmgnc argcnaarca rwsnwsnwsn gcngcnytnm gnaarttyat hgcngtntay   1440
ttygaytayw sntgygargg ngaygtnccn tgywsnytng ayytnwsnac naartayaar   1500
ytnatggayc ayytnccnga rytntgygcn cayytncayw snggngarca rgargtnytn   1560
ggncarcayc cnggncayws nwsnmgnmgn aaytayttym gnwsnaarws nggnmgnwsn   1620
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ytntaygtng cnathtgyaa yatgcaycar ttyathgayg argarccnga ytggttygar 1680
aarcarttya thccnttyca rcayccnccn gtnmgntayc argarccngt nytngaraar 1740
ttygaywsng gnytngtnyt naaygaygtn athwsnaarc cnggnccnga rwsngaytty 1800
tgymgnaarg tngargcntg ygtnytnggn gcngcnggnc cngcngayws ntaywsntay 1860
ytngarwsnc arcaygtngg nytngaycar gayacngarg cncarccnws ntgygaywsn 1920
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